

**WE CLAIM:**

1. A composition comprising:

(a) one, two, three, four or five isolated nucleic acids represented by SEQ ID NO:1; SEQ ID NO:2; SEQ ID NO:3; SEQ ID NO:5; and/or SEQ ID NO:6 (preferably all five nucleic acids are present); or fragments thereof that comprise at least about 10 contiguous nucleotides of said sequences, and/or

(b) one, two, three, four or five isolated nucleic acids represented by SEQ ID NO:31; SEQ ID NO:33; SEQ ID NO:34; SEQ ID NO:35; and/or SEQ ID NO:36; or fragments thereof that comprise at least about 10 contiguous nucleotides of said sequences, and/or

(c) one, two, three, four or five isolated nucleic acids represented by SEQ ID NO:61; SEQ ID NO:62; SEQ ID NO:64; SEQ ID NO:65; and/or SEQ ID NO:66; or fragments thereof that comprise at least about 10 contiguous nucleotides of said sequences, and/or

(d) one, two, three, four or five isolated nucleic acids represented by SEQ ID NO:91; SEQ ID NO:92; SEQ ID NO:93; SEQ ID NO:94; and/or SEQ ID NO:95; (preferably all five nucleic acids are present); or fragments thereof that comprise at least about 10 contiguous nucleotides of said sequences, and/or

(e) one, two, three, four or five isolated nucleic acids represented by SEQ ID NO:120; SEQ ID NO:121; SEQ ID NO:122; SEQ ID NO:123; and/or SEQ ID NO:125; or fragments thereof that comprise at least about 10 contiguous nucleotides of said sequences, and/or

(f) one or two isolated nucleic acids represented by SEQ ID NO:194 and/or SEQ ID NO:195, or fragments thereof that comprise at least about 10 contiguous nucleotides of said sequences.

2. The composition of claim 1, wherein each of (a), (b), (c), (d) and (e) comprises all five of the indicated nucleic acids and (f) comprises both of said nucleic acids.

3. The composition of claim 1, which is in the form of an aqueous solution.

4. The composition of claim 1, which is in the form of an array.

5. The array of claim 5, which comprises at least about 900 nucleic acids.

6. A composition comprising a set of two or more nucleic acid probes, each of which hybridizes with part or all of a coding sequence that is overexpressed in clear cell renal cell carcinoma (CC-RCC), papillary RCC, chromophobe/oncocytoma RCC, sarcomatoid RCC, TCC, or Wilms' tumors, which overexpression is based on comparison to a baseline value.

5 7. The composition of claim 6, wherein the baseline value is the expression of said coding sequence in normal renal tissue from (i) the subject from whom the tumor tissue is obtained or (ii) one or more normal individuals.

8. The composition of claim 7, which is in the form of an array.

9. The composition of claim 1 or 6, wherein one or more of the nucleic acids comprise  
10 nucleotides having at least one modified phosphate backbone selected from a phosphorothioate, a phosphoridothioate, a phosphoramidothioate, a phosphoramidate, a phosphordiimide, a methylphosphonate, an alkyl phosphotriester, 3'-aminopropyl, a formacetal, or an analogue thereof.

10. The array of claim 5 or claim 8, further comprising, bound to one or more nucleic acids  
15 of the array, one or more polynucleotides from a sample representing expressed genes, wherein the sample is from an individual subject's renal tumor, from normal tissue, or from both tumor and normal tissue.

11. The array of claim 5 or claim 8, wherein the nucleic acids of the array have been  
20 hybridized under conditions of high stringency to one or more polynucleotides from a sample representing expressed genes, wherein the sample is from an individual subject's renal tumor, from normal tissue, or from both tumor and normal tissue

13. The composition of claim 1 or claim 6, wherein the isolated nucleic acids are of mammalian origin.

14. The composition of claim 13, wherein the isolated nucleic acids are of human origin.

25 15. A composition comprising

- (a) one, two, three, four or five of the following isolated polypeptides: SEQ ID NO:196; SEQ ID NO:197; SEQ ID NO:198; SEQ ID NO:199 or 200; and/or SEQ ID NO:201, or antigenic fragments of said polypeptides, and/or

(b) one, two, three, four or five of the following isolated polypeptides: SEQ ID NO:221; SEQ ID NO:222; SEQ ID NO:223; SEQ ID NO:224; and/or SEQ ID NO:225, or antigenic fragments thereof, and/or

(c) one, two, three, four or five of the following isolated polypeptides: SEQ ID NO:248; SEQ ID NO:249; SEQ ID NO:250; SEQ ID NO:251; and/or SEQ ID NO:252, or antigenic fragments thereof, and/or

(d) one, two, three, four or five of the following isolated polypeptides: (i) a polypeptide encoded by an ORF that includes the nucleotide sequence SEQ ID NO:91 (ubiquitin thiolesterase); (ii) SEQ ID NO:271 or 272; (iii) SEQ ID NO:273; (iv) a polypeptide encoded by an ORF of SEQ ID NO:94 (*H. sapiens*  $\alpha$ -1 (VI) collagen); and/or (v) SEQ ID NO:274, or antigenic fragments thereof, and/or

(e) one, two, three, four or five polypeptides encoded by the following nucleic acids: (i) an ORF that includes SEQ ID NO:120 (keratin 14); (ii) SEQ ID NO:121 (collagen type VII,  $\alpha$ 1); (iii) SEQ ID NO:122 (keratin 19); (iv) SEQ ID NO:123 (plexin B3); and (v) SEQ ID NO:125 (integrin  $\beta$ 4); or antigenic fragments thereof, and/or

(f) one or two isolated polypeptides encoded by the nucleic acids SEQ ID NO:194 (heparin sulfate proteoglycan) and/or SEQ ID NO:195 (IGF II); or antigenic fragments thereof.

16. The composition of claim 16, wherein each of (a), (b), (c), (d) and (e) comprises all five of the indicated polypeptides, and (f) comprises both of said polypeptides.

17. A composition comprising antibodies specific for the polypeptides or fragments of the compositions of claim 15.

18. The composition of claim 19, which is in the form of an array.

19. A method for determining the subtype of a renal carcinoma in a subject, comprising

- (a) hybridizing nucleic acids of the composition of claim 1, under conditions of high stringency, to polynucleotides of a sample of the renal carcinoma; and
- (b) comparing the amount of the sample polynucleotides hybridized to said nucleic acids of the composition, to a baseline value,

wherein the amount of sample polynucleotide hybridized is indicative of the level of expression of the polynucleotide or polynucleotides in the renal tumor,

wherein said level of expression is characteristic of the subtype of renal carcinoma.

20. The method of claim 19, wherein the nucleic acid composition is in the form of an array.

21. The method claim 19 or 20, wherein,

(a) when the expression of said sample polynucleotide, as determined by its hybridization to one or more nucleic acids listed in Table 1, is up-regulated compared to the baseline value, the renal tumor is a clear cell-RCC;

(b) when the expression of said sample polynucleotide, as determined by its hybridization to one or more nucleic acids listed in Table 2, is up-regulated compared to the baseline value, the renal tumor is a papillary RCC;

(c) when the expression of said sample polynucleotide, as determined by its hybridization to one or more nucleic acids from Table 3, is up-regulated compared to the baseline value, the renal tumor is chromophobe-RCC/oncocytoma;

(d) when the expression of said sample polynucleotide, as determined by its hybridization to one or more nucleic acids listed in Table 5, is up-regulated compared to the baseline value, the renal tumor is a sarcomatoid-RCC;

(e) when the expression of said sample polynucleotide, as determined by its hybridization to one or more nucleic acids from Table 6, is up-regulated compared to the baseline value, the renal tumor is a transitional cell carcinoma; and

(f) when the expression of said sample polynucleotide, as reflected by its hybridization to one or more nucleic acids represented by SEQ ID NO:194 or SEQ ID NO:195, is up-regulated compared to the baseline value, the renal tumor is a Wilms' tumor.

22. The method of claim 19, wherein said sample polynucleotide is labeled with a detectable label.

23. The method of claim 22, wherein the detectable label is a fluorescent label.

24. A method for determining the subtype of a renal carcinoma in a subject, comprising

- (a) contacting the antibody composition of claim 17 with a polypeptide sample obtained from the renal carcinoma, under conditions effective for an antibody to bind specifically to a polypeptide; and
  - (b) comparing the amount of said binding, to a baseline value,
- 5 wherein the amount of binding of said sample polypeptide to said specific antibody or antibodies is indicative of the level of expression of the polypeptide in the renal tumor, wherein said level of expression is characteristic of the subtype of renal carcinoma.
25. A kit for detecting the presence and/or amount of a polynucleotide in a renal tumor sample, which is indicative of a subtype of renal carcinomas, comprising:
- 10 (a) the nucleic acid composition of claim 1 or 6; and, optionally,
- (b) one or more reagents that facilitate hybridization of nucleic acids of the composition to the sample polynucleotide, and/or that facilitate detection of the hybridized polynucleotide.
26. The kit of claim 25, wherein the nucleic acid composition is in the form of an array.
- 15 27. A kit for detecting the presence and/or amount of a polypeptide in a renal tumor sample, which is indicative of subtype of renal carcinoma, comprising:
- (a) the antibody composition of claim 17; and, optionally,
- (b) one or more reagents that facilitate binding of the antibodies of the composition to the sample polypeptide, and/or that facilitate detection of antibody binding.
- 20 28. The kit of claim 27, wherein the nucleic acid composition is in the form of an array.